



SEQUENCE LISTING

<110> CVITKOVITCH, Dennis

<120> SIGNAL PEPTIDES NUCLEIC ACID MOLECULES AND METHODS FOR TREATMENT OF CARIES

<130> 1889/00401

<140> 09/833,017

<141> 2001-04-10

<160> 30

<170> PatentIn version 3.0

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<212> DNA

<213> Streptococcus mutans

<220>

<221> CDS

<222> (1)..(141)

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Met Lys Lys Thr Leu Ser Leu Lys Asn Asp Phe Lys Glu Ile Lys Thr
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gat gaa tta gag att atc att ggc gga agc gga agc cta tca aca ttt 96
Asp Glu Leu Glu Ile Ile Ile Gly Gly Ser Gly Ser Leu Ser Thr Phe
20 25 30

ttc cgg ctg ttt aac aga agt ttt aca caa gct ttg gga aaa taa 141
Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys
35 40 45

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<211> 46

<212> PRT

<213> Streptococcus mutans

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Met Lys Lys Thr Leu Ser Leu Lys Asn Asp Phe Lys Glu Ile Lys Thr
1 5 10 15

Asp Glu Leu Glu Ile Ile Ile Gly Gly Ser Gly Ser Leu Ser Thr Phe
20 25 30

Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys
35 40 45

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 1 5 10 15
 caa gct ttg gga aaa 63
 Gln Ala Leu Gly Lys
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 Gln Ala Leu Gly Lys
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 1 5 10 15
 acc gtt cta ttt ctc ttg ttt cta ttt tct aag gta agt aat gtc act 96
 Thr Val Leu Phe Leu Leu Phe Leu Phe Ser Lys Val Ser Asn Val Thr
 20 25 30
 tta tcg aaa aag gaa tta act ctt ttt tcg ata agc aat ttt ctg ata 144
 Leu Ser Lys Lys Glu Leu Thr Leu Phe Ser Ile Ser Asn Phe Leu Ile
 35 40 45

atg att gct gtt acg atg gtg aac gta aac ctg ttt tat cct gca gag 192
Met Ile Ala Val Thr Met Val Asn Val Asn Leu Phe Tyr Pro Ala Glu
50 55 60

cct ctt tat ttt ata gct tta tca att tat ctt aat aga cag aat agt 240
Pro Leu Tyr Phe Ile Ala Leu Ser Ile Tyr Leu Asn Arg Gln Asn Ser
65 70 75 80

ctt tct cta aat ata ttt tat ggt ctg ctg cct gtt gcc agt tct gac 288
Leu Ser Leu Asn Ile Phe Tyr Gly Leu Leu Pro Val Ala Ser Ser Asp
85 90 95

ttg ttt agg cgg gca atc ata ttc ttt atc ttg gat gga act caa gga 336
Leu Phe Arg Arg Ala Ile Ile Phe Phe Ile Leu Asp Gly Thr Gln Gly
100 105 110

att gta atg ggc agt agc att ata acc acc tat atg atc gag ttt gca 384
Ile Val Met Gly Ser Ser Ile Ile Thr Thr Tyr Met Ile Glu Phe Ala
115 120 125

gga ata gcg cta agt tac ctc ttt ctc agt gtg ttc aat gtt gat att 432
Gly Ile Ala Leu Ser Tyr Leu Phe Leu Ser Val Phe Asn Val Asp Ile
130 135 140

ggt cga ctt aaa gat agt ttg acc aag atg aag gtc aaa aaa cgc ttg 480
Gly Arg Leu Lys Asp Ser Leu Thr Lys Met Lys Val Lys Lys Arg Leu
145 150 155 160

att cca atg aat att act atg ctt cta tac tac ctt tta ata cag gta 528
Ile Pro Met Asn Ile Thr Met Leu Leu Tyr Tyr Leu Leu Ile Gln Val
165 170 175

ttg tat gtt ata gag agt tat aat gtg ata ccg act tta aaa ttt cgt 576
Leu Tyr Val Ile Glu Ser Tyr Asn Val Ile Pro Thr Leu Lys Phe Arg
180 185 190

aaa ttt gtc gtt att gtc tat ctt att tta ttt ttg att ctg atc tca 624
Lys Phe Val Val Ile Val Tyr Leu Ile Leu Phe Leu Ile Leu Ile Ser
195 200 205

ttt tta agc caa tat acc aaa caa aag gtt caa aat gag ata atg gca 672
Phe Leu Ser Gln Tyr Thr Lys Gln Lys Val Gln Asn Glu Ile Met Ala
210 215 220

caa aag gaa gct cag att cga aat atc acc cag tat agt cag caa ata 720
Gln Lys Glu Ala Gln Ile Arg Asn Ile Thr Gln Tyr Ser Gln Gln Ile
225 230 235 240

gaa tct ctt tac aag gat att cga agt ttc cgc cat gat tat ctg aat 768
Glu Ser Leu Tyr Lys Asp Ile Arg Ser Phe Arg His Asp Tyr Leu Asn
245 250 255

att tta act agc ctc aga tta ggc att gaa aat aaa gat tta gct agt 816
Ile Leu Thr Ser Leu Arg Leu Gly Ile Glu Asn Lys Asp Leu Ala Ser
260 265 270

att gaa aag att tac cat caa atc tta gaa aaa aca gga cat caa ttg 864

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Ile Glu Lys Ile Tyr His Gln Ile Leu Glu Lys Thr Gly His Gln Leu
 275 280 285

cag gat acc cgt tat aat atc ggc cat cta gct aat att caa aac gat 912
 Gln Asp Thr Arg Tyr Asn Ile Gly His Leu Ala Asn Ile Gln Asn Asp
 290 295 300

gct gtc aag ggt atc ttg tca gca aaa atc tta gaa gct cag aat aaa 960
 Ala Val Lys Gly Ile Leu Ser Ala Lys Ile Leu Glu Ala Gln Asn Lys
 305 310 315 320

aag att gct gtc aat gta gaa gtc tca agt aaa ata caa ctg cct gag 1008
 Lys Ile Ala Val Asn Val Glu Val Ser Ser Lys Ile Gln Leu Pro Glu
 325 330 335

atg gag ttg ctt gat ttc att acc ata ctt tct atc ttg tgt gat aat 1056
 Met Glu Leu Leu Asp Phe Ile Thr Ile Leu Ser Ile Leu Cys Asp Asn
 340 345 350

gcc att gag gct gct ttc gaa tca tta aat cct gaa att cag tta gcc 1104
 Ala Ile Glu Ala Ala Phe Glu Ser Leu Asn Pro Glu Ile Gln Leu Ala
 355 360 365

ttt ttt aag aaa aat ggc agt ata gtc ttt atc att cag aat tcc acc 1152
 Phe Phe Lys Lys Asn Gly Ser Ile Val Phe Ile Ile Gln Asn Ser Thr
 370 375 380

aaa gaa aaa caa ata gat gtg agt aaa att ttt aaa gaa aac tat tcc 1200
 Lys Glu Lys Gln Ile Asp Val Ser Lys Ile Phe Lys Glu Asn Tyr Ser
 385 390 395 400

act aaa ggc tcc aat cgc ggt att ggt tta gca aag gtg aat cat att 1248
 Thr Lys Gly Ser Asn Arg Gly Ile Gly Leu Ala Lys Val Asn His Ile
 405 410 415

ctt gaa cat tat ccc aaa acc agt tta caa aca agc aat cat cat cat 1296
 Leu Glu His Tyr Pro Lys Thr Ser Leu Gln Thr Ser Asn His His His
 420 425 430

tta ttc aag caa ctc cta ata ata aaa tag 1326
 Leu Phe Lys Gln Leu Leu Ile Ile Lys
 435 440

<210> 6
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 <212> PRT
 <213> Streptococcus mutans

<400> 6

Met Asn Glu Ala Leu Met Ile Leu Ser Asn Gly Leu Leu Thr Tyr Leu
 1 5 10 15

Thr Val Leu Phe Leu Leu Phe Leu Phe Ser Lys Val Ser Asn Val Thr
 20 25 30

Cont

Leu Ser Lys Lys Glu Leu Thr Leu Phe Ser Ile Ser Asn Phe Leu Ile
35 40 45

Met Ile Ala Val Thr Met Val Asn Val Asn Leu Phe Tyr Pro Ala Glu
50 55 60

Pro Leu Tyr Phe Ile Ala Leu Ser Ile Tyr Leu Asn Arg Gln Asn Ser
65 70 75 80

Leu Ser Leu Asn Ile Phe Tyr Gly Leu Leu Pro Val Ala Ser Ser Asp
85 90 95

Leu Phe Arg Arg Ala Ile Ile Phe Phe Ile Leu Asp Gly Thr Gln Gly
100 105 110

Cont Ile Val Met Gly Ser Ser Ile Ile Thr Thr Tyr Met Ile Glu Phe Ala
115 120 125

Gly Ile Ala Leu Ser Tyr Leu Phe Leu Ser Val Phe Asn Val Asp Ile
130 135 140

Gly Arg Leu Lys Asp Ser Leu Thr Lys Met Lys Val Lys Lys Arg Leu
145 150 155 160

Ile Pro Met Asn Ile Thr Met Leu Leu Tyr Tyr Leu Leu Ile Gln Val
165 170 175

Leu Tyr Val Ile Glu Ser Tyr Asn Val Ile Pro Thr Leu Lys Phe Arg
180 185 190

Lys Phe Val Val Ile Val Tyr Leu Ile Leu Phe Leu Ile Leu Ile Ser
195 200 205

Phe Leu Ser Gln Tyr Thr Lys Gln Lys Val Gln Asn Glu Ile Met Ala
210 215 220

Gln Lys Glu Ala Gln Ile Arg Asn Ile Thr Gln Tyr Ser Gln Gln Ile
225 230 235 240

Glu Ser Leu Tyr Lys Asp Ile Arg Ser Phe Arg His Asp Tyr Leu Asn
245 250 255

Ile Leu Thr Ser Leu Arg Leu Gly Ile Glu Asn Lys Asp Leu Ala Ser
260 265 270

Ile Glu Lys Ile Tyr His Gln Ile Leu Glu Lys Thr Gly His Gln Leu
275 280 285

Gln Asp Thr Arg Tyr Asn Ile Gly His Leu Ala Asn Ile Gln Asn Asp
290 295 300

Ala Val Lys Gly Ile Leu Ser Ala Lys Ile Leu Glu Ala Gln Asn Lys
305 310 315 320

Lys Ile Ala Val Asn Val Glu Val Ser Ser Lys Ile Gln Leu Pro Glu
325 330 335

Met Glu Leu Leu Asp Phe Ile Thr Ile Leu Ser Ile Leu Cys Asp Asn
340 345 350

Ala Ile Glu Ala Ala Phe Glu Ser Leu Asn Pro Glu Ile Gln Leu Ala
355 360 365

Phe Phe Lys Lys Asn Gly Ser Ile Val Phe Ile Ile Gln Asn Ser Thr
370 375 380

Lys Glu Lys Gln Ile Asp Val Ser Lys Ile Phe Lys Glu Asn Tyr Ser
385 390 395 400

Thr Lys Gly Ser Asn Arg Gly Ile Gly Leu Ala Lys Val Asn His Ile
405 410 415

Leu Glu His Tyr Pro Lys Thr Ser Leu Gln Thr Ser Asn His His His
420 425 430

Leu Phe Lys Gln Leu Leu Ile Ile Lys
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<222> (1)..(750)

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ctt gaa acc acc att gca gct atc atg aaa gaa aaa aat tgg tct tat 96
Leu Glu Thr Thr Ile Ala Ala Ile Met Lys Glu Lys Asn Trp Ser Tyr
20 25 30

aaa gaa ttg act att ttt gga aaa cca caa caa ctt att gac gct atc 144
Lys Glu Leu Thr Ile Phe Gly Lys Pro Gln Gln Leu Ile Asp Ala Ile
35 40 45

cct gaa aag ggc aat cac cag att ttc ttt ttg gat att gaa atc aaa 192
Pro Glu Lys Gly Asn His Gln Ile Phe Phe Leu Asp Ile Glu Ile Lys
50 55 60

aaa gag gaa aag aaa gga ctg gaa gta gcc aat cag att aga cag cat 240
Lys Glu Glu Lys Lys Gly Leu Glu Val Ala Asn Gln Ile Arg Gln His
65 70 75 80

aat cct agt gca gtt att gtc ttt gtc acg aca cat tct gag ttt atg 288
Asn Pro Ser Ala Val Ile Val Phe Val Thr Thr His Ser Glu Phe Met
85 90 95

ccc ctc act ttt cag tat cag gta tct gct ttg gat ttt att gat aaa 336
Pro Leu Thr Phe Gln Tyr Gln Val Ser Ala Leu Asp Phe Ile Asp Lys
100 105 110

tct ttg aat cct gag gag ttc tcc cac cgc att gaa tca gcg ctg tat 384
Ser Leu Asn Pro Glu Glu Phe Ser His Arg Ile Glu Ser Ala Leu Tyr
115 120 125

tat gct atg gaa aac agc cag aag aat ggt caa tca gag gaa ctt ttt 432
Tyr Ala Met Glu Asn Ser Gln Lys Asn Gly Gln Ser Glu Glu Leu Phe
130 135 140

att ttc cat tca tct gaa act cag ttt cag gtc cct ttt gct gag att 480
Ile Phe His Ser Ser Glu Thr Gln Phe Gln Val Pro Phe Ala Glu Ile
145 150 155 160

ctg tat ttt gaa aca tct tca aca gcc cat aag ctc tgc ctt tat act 528
Leu Tyr Phe Glu Thr Ser Ser Thr Ala His Lys Leu Cys Leu Tyr Thr
165 170 175

tat gat gaa cgg att gaa ttc tac ggc agt atg act gac att gtt aaa 576
Tyr Asp Glu Arg Ile Glu Phe Tyr Gly Ser Met Thr Asp Ile Val Lys
180 185 190

atg gat aag aga ctt ttt cag tgc cat cgc tct ttt att gtc aat cct 624
Met Asp Lys Arg Leu Phe Gln Cys His Arg Ser Phe Ile Val Asn Pro
195 200 205

gcc aat att acc cgt att gat cgg aaa aaa cgc ttg gcc tat ttt cga 672
Ala Asn Ile Thr Arg Ile Asp Arg Lys Lys Arg Leu Ala Tyr Phe Arg
210 215 220

aat aat aag tct tgt ctt att tca cga act aag tta aca aaa ctg aga 720
 Asn Asn Lys Ser Cys Leu Ile Ser Arg Thr Lys Leu Thr Lys Leu Arg
 225 230 235 240

gct gtg att gct gat caa agg aga gca aaa 750
 Ala Val Ile Ala Asp Gln Arg Arg Ala Lys
 245 250

<210> 8
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 <212> PRT
 <213> Streptococcus mutans

<400> 8

Met Ile Ser Ile Phe Val Leu Glu Asp Asp Phe Leu Gln Gln Gly Arg
 1 5 10 15

Leu Glu Thr Thr Ile Ala Ala Ile Met Lys Glu Lys Asn Trp Ser Tyr
 20 25 30

Lys Glu Leu Thr Ile Phe Gly Lys Pro Gln Gln Leu Ile Asp Ala Ile
 35 40 45

Pro Glu Lys Gly Asn His Gln Ile Phe Phe Leu Asp Ile Glu Ile Lys
 50 55 60

Lys Glu Glu Lys Lys Gly Leu Glu Val Ala Asn Gln Ile Arg Gln His
 65 70 75 80

Asn Pro Ser Ala Val Ile Val Phe Val Thr Thr His Ser Glu Phe Met
 85 90 95

Pro Leu Thr Phe Gln Tyr Gln Val Ser Ala Leu Asp Phe Ile Asp Lys
 100 105 110

Ser Leu Asn Pro Glu Glu Phe Ser His Arg Ile Glu Ser Ala Leu Tyr
 115 120 125

Tyr Ala Met Glu Asn Ser Gln Lys Asn Gly Gln Ser Glu Glu Leu Phe
 130 135 140

Ile Phe His Ser Ser Glu Thr Gln Phe Gln Val Pro Phe Ala Glu Ile
 145 150 155 160

Chart

Leu Tyr Phe Glu Thr Ser Ser Thr Ala His Lys Leu Cys Leu Tyr Thr
165 170 175

Tyr Asp Glu Arg Ile Glu Phe Tyr Gly Ser Met Thr Asp Ile Val Lys
180 185 190

Met Asp Lys Arg Leu Phe Gln Cys His Arg Ser Phe Ile Val Asn Pro
195 200 205

Ala Asn Ile Thr Arg Ile Asp Arg Lys Lys Arg Leu Ala Tyr Phe Arg
210 215 220

Asn Asn Lys Ser Cys Leu Ile Ser Arg Thr Lys Leu Thr Lys Leu Arg
225 230 235 240

Ala Val Ile Ala Asp Gln Arg Arg Ala Lys
245 250

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<213> Streptococcus mutans

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<222> (1)..(46)

<400> 9

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Asp Glu Leu Glu Ile Ile Ile Gly Gly Ser Gly Ser Leu Ser Thr Phe
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Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys
35 40 45

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<213> Streptococcus mutans

<220>
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1 5 10 15

Asp Glu Leu Glu Ile Ile Ile Gly Gly Ser Gly Ser Leu Ser Thr Phe
20 25 30

Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys
35 40 45

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<212> PRT

<213> Streptococcus mutans

<220>

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<222> (1)..(46)

<400> 11

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1 5 10 15

Asp Glu Leu Glu Ile Ile Ile Gly Gly Ser Gly Ser Leu Ser Thr Phe
20 25 30

Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys
35 40 45

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<213> Streptococcus mutans

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<222> (1)..(43)

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1 5 10 15

Asp Glu Leu Glu Ile Ile Ile Gly Gly Ser Gly Thr Leu Ser Thr Phe
20 25 30

Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala
35 40

<210> 13

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<212> PRT

<213> Streptococcus mutans

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<222> (1)..(46)

<400> 13

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1 5 10 15

Asp Glu Leu Glu Ile Ile Ile Gly Gly Ser Gly Ser Leu Ser Thr Phe
20 25 30

Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys
35 40 45

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<222> (1)..(46)

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Asp Glu Leu Glu Ile Ile Ile Gly Gly Ser Gly Ser Leu Ser Thr Phe
20 25 30

Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys
35 40 45

<210> 15
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<212> PRT
<213> Streptococcus mutans

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<221> PEPTIDE
<222> (1)..(46)

<400> 15

Met Lys Lys Thr Leu Ser Leu Lys Asn Asp Phe Lys Glu Ile Lys Thr
1 5 10 15

Asp Glu Leu Glu Ile Ile Ile Gly Gly Ser Gly Ser Leu Ser Thr Phe
20 25 30

Phe Arg Leu Phe Asn Arg Ser Phe Thr Gln Ala Leu Gly Lys
35 40 45

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<220>
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<222> (1)..(21)

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Ser Gly Ser Leu Ser Thr Phe Phe Arg Leu Phe Asn Arg Ser Phe Thr
1 5 10 15

Gln Ala Leu Gly Lys
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<210> 17

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<212> DNA

<213> synthetic construct

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<221> PRIMER

<222> (1)..(19)

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<211> 20

<212> DNA

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<222> (1)..(20)

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<210> 19

<211> 24

<212> DNA

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<222> (1)..(24)

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<212> DNA

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<222> (1)..(21)

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<400> 21
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<210> 22
<211> 22
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<222> (1)..(22)

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<213> Streptococcus mutans

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aaaaaatgac tttaaagaaa ttaagactga tgaattagag attatcattg gcggaagcgg 180
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Conti

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<210> 24
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<212> DNA
<213> Streptococcus mutans

<220>
<221> CDS
<222> (1)..(408)

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1 5 10 15

tgg aaa tta agc cgt tat tac ttt att aaa atg tgg act cgt gaa gat 96
Trp Lys Leu Ser Arg Tyr Tyr Phe Ile Lys Met Trp Thr Arg Glu Asp
20 25 30

Cont
tgg caa caa gag gga atg ttg att ttg cac caa tta tta agg gaa cat 144
Trp Gln Gln Glu Gly Met Leu Ile Leu His Gln Leu Leu Arg Glu His
35 40 45

cca gaa tta gaa gag gat gat aca aaa ttg tat atc tat ttt aag aca 192
Pro Glu Leu Glu Glu Asp Asp Thr Lys Leu Tyr Ile Tyr Phe Lys Thr
50 55 60

cgt ttt tct aat tac att aaa gat gtt ttg cgt cag caa gaa agt cag 240
Arg Phe Ser Asn Tyr Ile Lys Asp Val Leu Arg Gln Gln Glu Ser Gln
65 70 75 80

aaa cgt cgt ttt aat aga atg tct tat gaa gaa gtc ggt gag att gaa 288
Lys Arg Arg Phe Asn Arg Met Ser Tyr Glu Glu Val Gly Glu Ile Glu
85 90 95

cac tgt ttg tca agt ggc ggt atg caa ttg gat gaa tat att tta ttt 336
His Cys Leu Ser Ser Gly Gly Met Gln Leu Asp Glu Tyr Ile Leu Phe
100 105 110

cgt gat agt ttg ctt gca tat aaa caa ggt ctg agt act gaa aag caa 384
Arg Asp Ser Leu Leu Ala Tyr Lys Gln Gly Leu Ser Thr Glu Lys Gln
115 120 125

gag ctg ttt gag cgc ttg gta gca ggagagcact ttttggaag gcaaagtatg 438

Glu Leu Phe Glu Arg Leu Val Ala
130 135

ctgaaagatt tacgtaaaaa attaagtgat tttaaggaaa aa

480

<210> 25
<211> 136
<212> PRT
<213> Streptococcus mutans

<400> 25

Met Glu Glu Asp Phe Glu Ile Val Phe Asn Lys Val Lys Pro Ile Val
1 5 10 15

Trp Lys Leu Ser Arg Tyr Tyr Phe Ile Lys Met Trp Thr Arg Glu Asp
20 25 30

Trp Gln Gln Glu Gly Met Leu Ile Leu His Gln Leu Leu Arg Glu His
35 40 45

Pro Glu Leu Glu Glu Asp Asp Thr Lys Leu Tyr Ile Tyr Phe Lys Thr
50 55 60

Arg Phe Ser Asn Tyr Ile Lys Asp Val Leu Arg Gln Gln Glu Ser Gln
65 70 75 80

Lys Arg Arg Phe Asn Arg Met Ser Tyr Glu Glu Val Gly Glu Ile Glu
85 90 95

His Cys Leu Ser Ser Gly Gly Met Gln Leu Asp Glu Tyr Ile Leu Phe
100 105 110

Arg Asp Ser Leu Leu Ala Tyr Lys Gln Gly Leu Ser Thr Glu Lys Gln
115 120 125

Glu Leu Phe Glu Arg Leu Val Ala
130 135

<210> 26
<211> 680
<212> DNA
<213> Streptococcus mutans

<220>
<221> misc_feature
<222> (1)..(680)

<400> 26
 gtaaataaaa cagccagtta agatgggaca tttatgtcct gttcttaaag tctttttcgt 60
 tttataataa ttttattata aaaggaggtc atcgtaatag atggaagaag attttgaaat 120
 tgtttttaat aagggttaagc caattgtatg gaaattaagc cgttattact ttattaaaat 180
 gtggactcgt gaagattggc aacaagaggg aatggtgatt ttgcaccaat tattaaggga 240
 acatccagaa ttagaagagg atgatacaaa attgtatatc tattttaaga cacgtttttc 300
 taattacatt aaagatgttt tgcgtcagca agaaagtcag aaacgtcgtt ttaatagaat 360
 gtcttatgaa gaagtcggtg agattgaaca ctgtttgtca agtggcggtg tgcaattgga 420
 tgaatatatt ttatttcgtg atagtttgct tgcataataa caaggtctga gtactgaaaa 480
 gcaagagctg tttgagcgtt tggtagcagg agagcacttt ttgggaaggc aaagtatgct 540
 gaaagattta cgtaaaaaat taagtgattt taaggaaaaa tagttaaaaa gggaaagaat 600
 ggaacatgtg attgtaccat tctttttggt tgaaaattaa gaaaagttat tataaattat 660
 tggtttaaca tgccatatta 680

<210> 27
 <211> 2280
 <212> DNA
 <213> Streptococcus mutans

<220>
 <221> CDS
 <222> (1)..(2280)

<400> 27
 atg aaa caa gtt att tat gtt gtt tta atc gtc ata gcc gtt aac att 48
 Met Lys Gln Val Ile Tyr Val Val Leu Ile Val Ile Ala Val Asn Ile
 1 5 10 15
 ctc tta gag att atc aaa aga gta aca aaa agg gga ggg aca gtt tcg 96
 Leu Leu Glu Ile Ile Lys Arg Val Thr Lys Arg Gly Gly Thr Val Ser
 20 25 30
 tca tct aat cct tta cca gat ggg cag tct aag ttg ttt tgg cgc aga 144
 Ser Ser Asn Pro Leu Pro Asp Gly Gln Ser Lys Leu Phe Trp Arg Arg
 35 40 45
 cat tat aag cta gta cct cag att gat acc aga gac tgt ggg ccg gca 192
 His Tyr Lys Leu Val Pro Gln Ile Asp Thr Arg Asp Cys Gly Pro Ala
 50 55 60
 gtg ctg gca tct gtt gca aag cat tac gga tct aat tac tct atc gct 240
 Val Leu Ala Ser Val Ala Lys His Tyr Gly Ser Asn Tyr Ser Ile Ala
 65 70 75 80

tat ctg cgg gaa ctc tca aag act aac aag cag gga aca aca gct ctt	288
Tyr Leu Arg Glu Leu Ser Lys Thr Asn Lys Gln Gly Thr Thr Ala Leu	
85 90 95	

ggc att gtt gaa gct gct aaa aag tta ggc ttt gaa aca cgc tct atc	336
Gly Ile Val Glu Ala Ala Lys Lys Leu Gly Phe Glu Thr Arg Ser Ile	
100 105 110	

aag gcg gat atg acg ctt ttt gat tat aat gat ttg acc tat cct ttt	384
Lys Ala Asp Met Thr Leu Phe Asp Tyr Asn Asp Leu Thr Tyr Pro Phe	
115 120 125	

atc gtc cat gtg att aaa gga aaa cgt ctg cag cat tat tat gtc gtc	432
Ile Val His Val Ile Lys Gly Lys Arg Leu Gln His Tyr Tyr Val Val	
130 135 140	

tat ggc agc cag aat aat cag ctg att att gga gat cct gat cct tca	480
Tyr Gly Ser Gln Asn Asn Gln Leu Ile Ile Gly Asp Pro Asp Pro Ser	
145 150 155 160	

gtt aag gtg act agg atg agt aag gaa cgc ttt caa tca gag tgg aca	528
Val Lys Val Thr Arg Met Ser Lys Glu Arg Phe Gln Ser Glu Trp Thr	
165 170 175	

ggc ctt gca att ttc cta gct cct cag cct aac tat aag cct cat aaa	576
Gly Leu Ala Ile Phe Leu Ala Pro Gln Pro Asn Tyr Lys Pro His Lys	
180 185 190	

ggt gaa aaa aat ggt ttg tct aat ttc ttc ccg ttg atc ttt aag cag	624
Gly Glu Lys Asn Gly Leu Ser Asn Phe Phe Pro Leu Ile Phe Lys Gln	
195 200 205	

aaa gct ttg atg act tat att atc ata gct agc ttg att gtg acg ctc	672
Lys Ala Leu Met Thr Tyr Ile Ile Ile Ala Ser Leu Ile Val Thr Leu	
210 215 220	

att gat att gtc gga tca tac tat ctc caa gga ata ttg gac gag tac	720
Ile Asp Ile Val Gly Ser Tyr Tyr Leu Gln Gly Ile Leu Asp Glu Tyr	
225 230 235 240	

att cct gat cag ctg att tca act tta gga atg att acg att ggt ctg	768
Ile Pro Asp Gln Leu Ile Ser Thr Leu Gly Met Ile Thr Ile Gly Leu	
245 250 255	

ata ata acc tat att atc cag cag gtc atg gct ttt gca aaa gaa tac	816
Ile Ile Thr Tyr Ile Ile Gln Gln Val Met Ala Phe Ala Lys Glu Tyr	
260 265 270	

ctc ttg gcc gta ctc agt ttg cgt tta gtc att gat gtt atc ctg tct	864
Leu Leu Ala Val Leu Ser Leu Arg Leu Val Ile Asp Val Ile Leu Ser	
275 280 285	

tat atc aaa cat att ttt acg ctt cct atg tct ttc ttt gcg aca agg	912
Tyr Ile Lys His Ile Phe Thr Leu Pro Met Ser Phe Phe Ala Thr Arg	
290 295 300	

cga aca gga gaa atc acg tct cgt ttt aca gat gcc aat cag att att	960
---	-----

Arg Thr Gly Glu Ile Thr Ser Arg Phe Thr Asp Ala Asn Gln Ile Ile
 305 310 315 320
 gat gct gta gcg tca acc atc ttt tca atc ttt tta gat atg act atg 1008
 Asp Ala Val Ala Ser Thr Ile Phe Ser Ile Phe Leu Asp Met Thr Met
 325 330 335
 gta att ttg gtt ggt ggg gtt ttg ttg gcg caa aac aat aac ctt ttc 1056
 Val Ile Leu Val Gly Gly Val Leu Leu Ala Gln Asn Asn Asn Leu Phe
 340 345 350
 ttt cta acc ttg ctc tcc att ccg att tat gcc atc att att ttt gct 1104
 Phe Leu Thr Leu Leu Ser Ile Pro Ile Tyr Ala Ile Ile Ile Phe Ala
 355 360 365
 ttc ttg aaa ccc ttt gag aaa atg aat cac gaa gtg atg gaa agc aat 1152
 Phe Leu Lys Pro Phe Glu Lys Met Asn His Glu Val Met Glu Ser Asn
 370 375 380
 gct gtg gta agt tct tct atc att gaa gat atc aat ggg atg gaa acc 1200
 Ala Val Val Ser Ser Ser Ile Ile Glu Asp Ile Asn Gly Met Glu Thr
 385 390 395 400
 att aaa tca ctc aca agt gag tcc gct cgt tat caa aac att gat agt 1248
 Ile Lys Ser Leu Thr Ser Glu Ser Ala Arg Tyr Gln Asn Ile Asp Ser
 405 410 415
 gaa ttt gtt gat tat ttg gag aaa aac ttt aag cta cac aag tat agt 1296
 Glu Phe Val Asp Tyr Leu Glu Lys Asn Phe Lys Leu His Lys Tyr Ser
 420 425 430
 gcc att caa acc gca tta aaa agc ggt gct aag ctt atc ctc aat gtt 1344
 Ala Ile Gln Thr Ala Leu Lys Ser Gly Ala Lys Leu Ile Leu Asn Val
 435 440 445
 gtc att ctc tgg tat ggc tct cgt cta gtt atg gat aat aaa atc tca 1392
 Val Ile Leu Trp Tyr Gly Ser Arg Leu Val Met Asp Asn Lys Ile Ser
 450 455 460
 gtt ggt cag ctt atc acc ttt aat gct ttg ctg tct tat ttc tca aat 1440
 Val Gly Gln Leu Ile Thr Phe Asn Ala Leu Leu Ser Tyr Phe Ser Asn
 465 470 475 480
 cca att gaa aat att atc aat ctg caa tcc aaa ctg cag tca gct cgc 1488
 Pro Ile Glu Asn Ile Ile Asn Leu Gln Ser Lys Leu Gln Ser Ala Arg
 485 490 495
 gtt gcc aat aca cgt ctt aat gag gtc tat ctt gtc gaa tct gaa ttt 1536
 Val Ala Asn Thr Arg Leu Asn Glu Val Tyr Leu Val Glu Ser Glu Phe
 500 505 510
 gaa aaa gac ggc gat tta tca gaa aat agc ttt tta gat ggt gat att 1584
 Glu Lys Asp Gly Asp Leu Ser Glu Asn Ser Phe Leu Asp Gly Asp Ile
 515 520 525
 tcg ttt gaa aat ctt tct tat aaa tat gga ttt ggg cga gat acc tta 1632
 Ser Phe Glu Asn Leu Ser Tyr Lys Tyr Gly Phe Gly Arg Asp Thr Leu

Cont

530	535	540	
tca gat att aat tta	tca atc aaa aaa ggc	tcc aag gtc agt cta gtt	1680
Ser Asp Ile Asn Leu	Ser Ile Lys Lys Gly	Ser Lys Val Ser Leu Val	
545	550	555 560	
gga gcc agt ggt tct	ggt aaa aca act ttg	gct aaa ctg att gtc aat	1728
Gly Ala Ser Gly Ser	Gly Lys Thr Thr Leu	Ala Lys Leu Ile Val Asn	
565	570	575	
ttc tac gag cct aac	aag ggg att gtt cga	atc aat ggc aat gat tta	1776
Phe Tyr Glu Pro Asn	Lys Gly Ile Val Arg	Ile Asn Gly Asn Asp Leu	
580	585	590	
aaa gtt att gat aag	aca gct ttg cgg cgg	cat att agc tat ttg ccg	1824
Lys Val Ile Asp Lys	Thr Ala Leu Arg Arg	His Ile Ser Tyr Leu Pro	
595	600	605	
caa cag gcc tat gtt	ttt agt ggc tct att	atg gat aat ctc gtt tta	1872
Gln Gln Ala Tyr Val	Phe Ser Gly Ser Ile	Met Asp Asn Leu Val Leu	
610	615	620	
gga gct aaa gaa gga	acg agt cag gaa gac	att att cgt gct tgt gaa	1920
Gly Ala Lys Glu Gly	Thr Ser Gln Glu Asp	Ile Ile Arg Ala Cys Glu	
625	630	635 640	
att gct gaa atc cgc	tcg gac att gaa caa	atg cct cag ggc tat cag	1968
Ile Ala Glu Ile Arg	Ser Asp Ile Glu Gln	Met Pro Gln Gly Tyr Gln	
645	650	655	
aca gag tta tca gat	ggt gcc ggt att tct	ggc ggt caa aaa cag cgg	2016
Thr Glu Leu Ser Asp	Gly Ala Gly Ile Ser	Gly Gly Gln Lys Gln Arg	
660	665	670	
att gct tta gct agg	gcc tta tta aca cag	gca ccg gtt ttg att ctg	2064
Ile Ala Leu Ala Arg	Ala Leu Leu Thr Gln	Ala Pro Val Leu Ile Leu	
675	680	685	
gat gaa gcc acc agc	agt ctt gat att ttg	aca gaa aag aaa att atc	2112
Asp Glu Ala Thr Ser	Ser Ser Leu Asp Ile	Leu Thr Glu Lys Lys Ile Ile	
690	695	700	
agc aat ctc tta cag	atg acg gag aaa aca	ata att ttt gtt gcc cac	2160
Ser Asn Leu Leu Gln	Met Thr Glu Lys Thr	Ile Ile Phe Val Ala His	
705	710	715 720	
cgc tta agc att tca	cag cgt act gac gaa	gtc att gtc atg gat cag	2208
Arg Leu Ser Ile Ser	Gln Arg Thr Asp Glu	Val Ile Val Met Asp Gln	
725	730	735	
gga aaa att gtt gaa	caa ggc act cat aag	gaa ctt tta gct aag caa	2256
Gly Lys Ile Val Glu	Gln Gly Thr His Lys	Glu Leu Leu Ala Lys Gln	
740	745	750	
ggt ttc tat tat aac	ctg ttt aat		2280
Gly Phe Tyr Tyr Asn	Leu Phe Asn		
755	760		

Cont

<210> 28
<211> 760
<212> PRT
<213> Streptococcus mutans

<400> 28

Met Lys Gln Val Ile Tyr Val Val Leu Ile Val Ile Ala Val Asn Ile
1 5 10 15

Leu Leu Glu Ile Ile Lys Arg Val Thr Lys Arg Gly Gly Thr Val Ser
20 25 30

Ser Ser Asn Pro Leu Pro Asp Gly Gln Ser Lys Leu Phe Trp Arg Arg
35 40 45

His Tyr Lys Leu Val Pro Gln Ile Asp Thr Arg Asp Cys Gly Pro Ala
50 55 60

Val Leu Ala Ser Val Ala Lys His Tyr Gly Ser Asn Tyr Ser Ile Ala
65 70 75 80

Cont
Tyr Leu Arg Glu Leu Ser Lys Thr Asn Lys Gln Gly Thr Thr Ala Leu
85 90 95

Gly Ile Val Glu Ala Ala Lys Lys Leu Gly Phe Glu Thr Arg Ser Ile
100 105 110

Lys Ala Asp Met Thr Leu Phe Asp Tyr Asn Asp Leu Thr Tyr Pro Phe
115 120 125

Ile Val His Val Ile Lys Gly Lys Arg Leu Gln His Tyr Tyr Val Val
130 135 140

Tyr Gly Ser Gln Asn Asn Gln Leu Ile Ile Gly Asp Pro Asp Pro Ser
145 150 155 160

Val Lys Val Thr Arg Met Ser Lys Glu Arg Phe Gln Ser Glu Trp Thr
165 170 175

Gly Leu Ala Ile Phe Leu Ala Pro Gln Pro Asn Tyr Lys Pro His Lys
180 185 190

Gly Glu Lys Asn Gly Leu Ser Asn Phe Phe Pro Leu Ile Phe Lys Gln
195 200 205

Lys Ala Leu Met Thr Tyr Ile Ile Ile Ala Ser Leu Ile Val Thr Leu
210 215 220

Ile Asp Ile Val Gly Ser Tyr Tyr Leu Gln Gly Ile Leu Asp Glu Tyr
225 230 235 240

Ile Pro Asp Gln Leu Ile Ser Thr Leu Gly Met Ile Thr Ile Gly Leu
245 250 255

Ile Ile Thr Tyr Ile Ile Gln Gln Val Met Ala Phe Ala Lys Glu Tyr
260 265 270

Leu Leu Ala Val Leu Ser Leu Arg Leu Val Ile Asp Val Ile Leu Ser
275 280 285

Tyr Ile Lys His Ile Phe Thr Leu Pro Met Ser Phe Phe Ala Thr Arg
290 295 300

Arg Thr Gly Glu Ile Thr Ser Arg Phe Thr Asp Ala Asn Gln Ile Ile
305 310 315 320

Cont Asp Ala Val Ala Ser Thr Ile Phe Ser Ile Phe Leu Asp Met Thr Met
325 330 335

Val Ile Leu Val Gly Gly Val Leu Leu Ala Gln Asn Asn Asn Leu Phe
340 345 350

Phe Leu Thr Leu Leu Ser Ile Pro Ile Tyr Ala Ile Ile Ile Phe Ala
355 360 365

Phe Leu Lys Pro Phe Glu Lys Met Asn His Glu Val Met Glu Ser Asn
370 375 380

Ala Val Val Ser Ser Ser Ile Ile Glu Asp Ile Asn Gly Met Glu Thr
385 390 395 400

Ile Lys Ser Leu Thr Ser Glu Ser Ala Arg Tyr Gln Asn Ile Asp Ser
405 410 415

Glu Phe Val Asp Tyr Leu Glu Lys Asn Phe Lys Leu His Lys Tyr Ser

420

425

430

Ala Ile Gln Thr Ala Leu Lys Ser Gly Ala Lys Leu Ile Leu Asn Val
 435 440 445

Val Ile Leu Trp Tyr Gly Ser Arg Leu Val Met Asp Asn Lys Ile Ser
 450 455 460

Val Gly Gln Leu Ile Thr Phe Asn Ala Leu Leu Ser Tyr Phe Ser Asn
 465 470 475 480

Pro Ile Glu Asn Ile Ile Asn Leu Gln Ser Lys Leu Gln Ser Ala Arg
 485 490 495

Val Ala Asn Thr Arg Leu Asn Glu Val Tyr Leu Val Glu Ser Glu Phe
 500 505 510

Glu Lys Asp Gly Asp Leu Ser Glu Asn Ser Phe Leu Asp Gly Asp Ile
 515 520 525

Ser Phe Glu Asn Leu Ser Tyr Lys Tyr Gly Phe Gly Arg Asp Thr Leu
 530 535 540

Ser Asp Ile Asn Leu Ser Ile Lys Lys Gly Ser Lys Val Ser Leu Val
 545 550 555 560

Gly Ala Ser Gly Ser Gly Lys Thr Thr Leu Ala Lys Leu Ile Val Asn
 565 570 575

Phe Tyr Glu Pro Asn Lys Gly Ile Val Arg Ile Asn Gly Asn Asp Leu
 580 585 590

Cont
 Lys Val Ile Asp Lys Thr Ala Leu Arg Arg His Ile Ser Tyr Leu Pro
 595 600 605

Gln Gln Ala Tyr Val Phe Ser Gly Ser Ile Met Asp Asn Leu Val Leu
 610 615 620

Gly Ala Lys Glu Gly Thr Ser Gln Glu Asp Ile Ile Arg Ala Cys Glu
 625 630 635 640

Ile Ala Glu Ile Arg Ser Asp Ile Glu Gln Met Pro Gln Gly Tyr Gln
 645 650 655

Thr Glu Leu Ser Asp Gly Ala Gly Ile Ser Gly Gly Gln Lys Gln Arg
660 665 670

Ile Ala Leu Ala Arg Ala Leu Leu Thr Gln Ala Pro Val Leu Ile Leu
675 680 685

Asp Glu Ala Thr Ser Ser Leu Asp Ile Leu Thr Glu Lys Lys Ile Ile
690 695 700

Ser Asn Leu Leu Gln Met Thr Glu Lys Thr Ile Ile Phe Val Ala His
705 710 715 720

Arg Leu Ser Ile Ser Gln Arg Thr Asp Glu Val Ile Val Met Asp Gln
725 730 735

Gly Lys Ile Val Glu Gln Gly Thr His Lys Glu Leu Leu Ala Lys Gln
740 745 750

Gly Phe Tyr Tyr Asn Leu Phe Asn
755 760

<210> 29
<211> 900
<212> DNA
<213> Streptococcus mutans

<220>
<221> CDS
<222> (1)..(900)

<400> 29
atg gat cct aaa ttt tta caa agt gca gaa ttt tat agg aga cgc tat 48
Met Asp Pro Lys Phe Leu Gln Ser Ala Glu Phe Tyr Arg Arg Arg Tyr
1 5 10 15

cat aat ttt gcg aca cta tta att gtt cct ttg gtc tgc ttg att atc 96
His Asn Phe Ala Thr Leu Leu Ile Val Pro Leu Val Cys Leu Ile Ile
20 25 30

ttc ttg gtc ata ttc ctt tgt ttt gct aaa aaa gaa att aca gtg att 144
Phe Leu Val Ile Phe Leu Cys Phe Ala Lys Lys Glu Ile Thr Val Ile
35 40 45

tct act ggt gaa gtt gca cca aca aag gtt gta gat gtt atc caa tct 192
Ser Thr Gly Glu Val Ala Pro Thr Lys Val Val Asp Val Ile Gln Ser
50 55 60

tac agt gac agt tca atc att aaa aat aat tta gat aat aat gca gct 240

Scat

Tyr Ser Asp Ser Ser Ile Ile Lys Asn Asn Leu Asp Asn Asn Ala Ala
65 70 75 80

gtt gag aag gga gac gtt tta att gaa tat tca gaa aat gcc agt cca 288
Val Glu Lys Gly Asp Val Leu Ile Glu Tyr Ser Glu Asn Ala Ser Pro
85 90 95

aac cgt cag act gaa caa aag aat att ata aaa gaa aga caa aaa cga 336
Asn Arg Gln Thr Glu Gln Lys Asn Ile Ile Lys Glu Arg Gln Lys Arg
100 105 110

gaa gag aag gaa aag aaa aaa cac caa aag agc aag aaa aag aag aag 384
Glu Glu Lys Glu Lys Lys Lys His Gln Lys Ser Lys Lys Lys Lys Lys
115 120 125

tct aag agc aag aaa gct tcc aaa gat aag aaa aag aaa tcg aaa gac 432
Ser Lys Ser Lys Lys Ala Ser Lys Asp Lys Lys Lys Lys Ser Lys Asp
130 135 140

aag gaa agc agc tct gac gat gaa aat gag aca aaa aag gtt tcg att 480
Lys Glu Ser Ser Ser Asp Asp Glu Asn Glu Thr Lys Lys Val Ser Ile
145 150 155 160

ttt gct tca gaa gat ggt att att cat acc aat ccc aaa tat gat ggt 528
Phe Ala Ser Glu Asp Gly Ile Ile His Thr Asn Pro Lys Tyr Asp Gly
165 170 175

gcc aat att att ccg aag caa acc gag att gct caa atc tat cct gat 576
Ala Asn Ile Ile Pro Lys Gln Thr Glu Ile Ala Gln Ile Tyr Pro Asp
180 185 190

att caa aaa aca aga aaa gtg tta atc acc tat tat gct tct tct gat 624
Ile Gln Lys Thr Arg Lys Val Leu Ile Thr Tyr Tyr Ala Ser Ser Asp
195 200 205

gat gtt gtt tct atg aaa aag ggg caa acc gct cgt ctt tcc ttg gaa 672
Asp Val Val Ser Met Lys Lys Gly Gln Thr Ala Arg Leu Ser Leu Glu
210 215 220

aaa aag gga aat gac aag gtt gtt att gaa gga aaa att aac aat gtc 720
Lys Lys Gly Asn Asp Lys Val Val Ile Glu Gly Lys Ile Asn Asn Val
225 230 235 240

gct tca tca gca act act act aaa aaa gga aat ctc ttt aag gtt act 768
Ala Ser Ser Ala Thr Thr Thr Lys Lys Gly Asn Leu Phe Lys Val Thr
245 250 255

gcc aaa gta aag gtt tct aag aaa aat agc aaa ctc atc aag tat ggt 816
Ala Lys Val Lys Val Ser Lys Lys Asn Ser Lys Leu Ile Lys Tyr Gly
260 265 270

atg aca ggc aag aca gtc act gtc att gat aaa aag act tat ttt gat 864
Met Thr Gly Lys Thr Val Thr Val Ile Asp Lys Lys Thr Tyr Phe Asp
275 280 285

tat ttc aaa gat aaa tta ctg cat aaa atg gat aat 900
Tyr Phe Lys Asp Lys Leu Leu His Lys Met Asp Asn

Cont

290

295

300

<210> 30
 <211> 300
 <212> PRT
 <213> Streptococcus mutans

<400> 30

Met Asp Pro Lys Phe Leu Gln Ser Ala Glu Phe Tyr Arg Arg Arg Tyr
 1 5 10 15

His Asn Phe Ala Thr Leu Leu Ile Val Pro Leu Val Cys Leu Ile Ile
 20 25 30

Phe Leu Val Ile Phe Leu Cys Phe Ala Lys Lys Glu Ile Thr Val Ile
 35 40 45

Ser Thr Gly Glu Val Ala Pro Thr Lys Val Val Asp Val Ile Gln Ser
 50 55 60

Cont
 Tyr Ser Asp Ser Ser Ile Ile Lys Asn Asn Leu Asp Asn Asn Ala Ala
 65 70 75 80

Val Glu Lys Gly Asp Val Leu Ile Glu Tyr Ser Glu Asn Ala Ser Pro
 85 90 95

Asn Arg Gln Thr Glu Gln Lys Asn Ile Ile Lys Glu Arg Gln Lys Arg
 100 105 110

Glu Glu Lys Glu Lys Lys Lys His Gln Lys Ser Lys Lys Lys Lys Lys
 115 120 125

Ser Lys Ser Lys Lys Ala Ser Lys Asp Lys Lys Lys Lys Ser Lys Asp
 130 135 140

Lys Glu Ser Ser Ser Asp Asp Glu Asn Glu Thr Lys Lys Val Ser Ile
 145 150 155 160

Phe Ala Ser Glu Asp Gly Ile Ile His Thr Asn Pro Lys Tyr Asp Gly
 165 170 175

Ala Asn Ile Ile Pro Lys Gln Thr Glu Ile Ala Gln Ile Tyr Pro Asp
 180 185 190

Ile Gln Lys Thr Arg Lys Val Leu Ile Thr Tyr Tyr Ala Ser Ser Asp
195 200 205

Asp Val Val Ser Met Lys Lys Gly Gln Thr Ala Arg Leu Ser Leu Glu
210 215 220

Lys Lys Gly Asn Asp Lys Val Val Ile Glu Gly Lys Ile Asn Asn Val
225 230 235 240

Ala Ser Ser Ala Thr Thr Thr Lys Lys Gly Asn Leu Phe Lys Val Thr
245 250 255

Ala Lys Val Lys Val Ser Lys Lys Asn Ser Lys Leu Ile Lys Tyr Gly
260 265 270

Met Thr Gly Lys Thr Val Thr Val Ile Asp Lys Lys Thr Tyr Phe Asp
275 280 285

Chanc. Tyr Phe Lys Asp Lys Leu Leu His Lys Met Asp Asn
290 295 300
